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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software.

In case of problems, please read the online BLAST help.
If your question is not covered, please contact <helpdesk@expasy.org>.

NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

==========

Query: 30 AA
Date run: 2005-10-27 21:09:24 UTC+0100 on sib-gm1.unil.ch
Program: NCBI BLASTP 1.5.4-Paracel [2003-06-05]
Database: EXPASY/UniProtKB
2,482,761 sequences; 813,543,939 total letters
UniProt Knowledgebase Release 6.3 consists of:
UniProtKB/Swiss-Prot Release 48.3 of 25-Oct-2005: 196277 entries
UniProtKB/TrEMBL Release 31.3 of 25-Oct-2005: 2273976 entries

Taxonomic view | NiceBlast view | Printable view

List of potentially matching sequences

Send selected sequences to Clustal W (multiple alignment) Submit Query
Select up to...

☐ Include query sequence

	Db	AC	Description	Score	E-value
☐	tr	Q83U44	_CLOPE Beta2-toxin [cpb2] [Clostridium perfringens]	95	2e-19
☐	tr	Q4ZFT7	_CLOPE Beta2 toxin [Clostridium perfringens]	95	2e-19
☐	tr	Q4ZFT6	_CLOPE Beta2 toxin [Clostridium perfringens]	95	2e-19
☐	tr	O86264	_CLOPE Beta 2 toxin precursor [Clostridium perfringens C]	95	2e-19
☐	tr	Q93MD0	_CLOPE Beta2-toxin [cpb2] [Clostridium perfringens]	89	1e-17
☐	tr	Q4ZFT4	_CLOPE Beta2 toxin [Clostridium perfringens]	88	3e-17
☐	tr	Q50NG8	_ENTHI Receptor protein kinase, putative [442.t00003] [...	48	3e-05
☐	tr	Q72MW1	_LEPIC Hypothetical protein [LIC13078] [Leptospira inte...	36	0.083
☐	tr	Q4AAS7	_MYCHJ Signal peptidase I (EC 3.4.21.89) [sipS] [Mycopl...	35	0.20

☐	tr Q5HX88	_CAMJR Cytolethal distending toxin, subunit C [cdtC] [C...	35	0.27
☐	tr Q46102	_CAMJE CdtC (Cytolethal distending toxin C) [cdtC] [Cam...	35	0.27
☐	tr Q7B3S5	_CAMJE CdtC protein (Fragment) [cdtC] [Campylobacter je...	35	0.27
☐	tr Q5F1K4	_CAMJE Cytolethal distending toxin C [cdtC] [Campylobac...	35	0.27
☐	tr O33865	_BACPU Plasmid pSH1452, Rep [Bacillus pumilus (Bacillus...	35	0.27
☐	sp P04660	HEMA_IADNY Hemagglutinin precursor [Contains: Hemagglu...	34	0.48
☐	tr Q81L65	_BACAN Iron compound ABC transporter, iron compound-bin...	34	0.48
☐	tr Q894Q1	_CLOTE Membrane associated protein [CTC01484] [Clostrid...	33	0.87
☐	tr Q4A8Y6	_MYCH7 Signal peptidase I (EC 3.4.21.89) [sipS] [Mycopl...	33	0.87
☐	tr Q54JE1	_DICDI Hypothetical protein [DDB0187788] [Dictyostelium...	32	1.2
☐	tr Q52TF1	_CAMJE Cytolethal distending toxin C (Fragment) [cdtC] ...	32	1.6
☐	tr Q52TF0	_CAMJE Cytolethal distending toxin C (Fragment) [cdtC] ...	32	1.6
☐	sp P45963	ACR7_CAEEL Acetylcholine receptor, alpha-type subunit ...	32	2.1
☐	tr Q8EZK0	_LEPIN Hypothetical protein [LA3853] [Leptospira interr...	32	2.1
☐	tr Q731T5	_BACC1 HlyC domain protein [BCE4080] [Bacillus cereus (...	32	2.1
☐	tr Q41GQ2	_9BACI Binding-protein-dependent transport systems inne...	32	2.1
☐	tr O59092	_PYRHO Hypothetical protein PH1367 [PH1367] [Pyrococcus...	32	2.1
☐	tr Q8TID2	_METAC Predicted protein [MA4221] [Methanosarcina aceti...	32	2.1
☐	sp Q98KB0	MRAY_RHILO Phospho-N-acetylmuramoyl-pentapeptide-trans...	31	2.8
☐	tr Q8AWN0	_9SMEG Rhodopsin (Fragment) [Rhod] [Spinachia spinachia]	31	2.8
☐	tr Q7YTK2	_CAEEL Hypothetical protein [W01D2.6] [Caenorhabditis e...	31	2.8
☐	tr Q4IBS5	_GIBZE Hypothetical protein [FG05333.1] [Gibberella zea...	31	2.8
☐	sp P87245	KMS1_SCHPO Karyogamy meiotic segregation protein 1 [km...	31	3.8
☐	tr Q897V9	_CLOTE Hypothetical protein [CTC00614] [Clostridium tet...	31	3.8
☐	tr Q488C5	_COLP3 Arylsulfatase (EC 3.1.6.1) [atsA] [Colwellia psy...	31	3.8
☐	tr Q4YW58	_PLABE Hypothetical protein [PB000503.02.0] [Plasmodium...	31	3.8
☐	tr Q4XSE9	_PLACH Hypothetical protein [PC000754.03.0] [Plasmodium...	31	3.8
☐	tr O45280	_CAEEL Hypothetical protein srbc-83 [srbc-83] [Caenorha...	31	3.8
☐	tr Q6CS24	_KLULA Similar to sp|P25371 Saccharomyces cerevisiae YC...	31	3.8
☐	tr Q3T6M7	_9PERO Rhodopsin (Fragment) [Archoplites interruptus]	30	5.1
☐	tr Q3T6M3	_9PERO Rhodopsin (Fragment) [Enneacanthus obesus]	30	5.1
☐	tr Q3QJ06	_9GAMM Protein-disulfide reductase precursor (EC 1.8.1....	30	5.1
☐	tr Q3NFU5	_9HELI Cytochrome c, class I precursor [TmdenDRAFT_1375...	30	5.1
☐	tr Q5ZGC8	_9VIRU Transmembrane glycoprotein [PHG11b_49] [Bacterio...	30	5.1
☐	tr Q61RZ6	_CAEBR Hypothetical protein CBG06382 [CBG06382] [Caenor...	30	5.1
☐	tr Q6YMD9	_9HEMI Cytochrome oxidase subunit I (Fragment) [COI] [L...	30	5.1
☐	tr Q50SK5	_ENTHI Hypothetical protein [256.t00009] [Entamoeba his...	30	5.1
☐	tr Q8U1W2	_PYRFU Hypothetical protein PF1092 [PF1092] [Pyrococcus...	30	5.1
☐	tr Q91F76	_IRV6 450L [Chilo iridescent virus (CIV) (Insect irides...	30	6.8
☐	tr Q8QLT2	_9INFA Non structural protein 1 [NS1] [Influenza A viru...	30	6.8
☐	tr Q8Y8R0	_LISMO Putative peptidoglycan bound protein (LPXTG moti...	30	6.8
☐	tr Q6HR76	_BACAN Hypothetical protein [BAS4921] [Bacillus anthracis]	30	6.8
☐	tr Q4EVA3	_LISMO Cell wall surface anchor family protein [LMOf685...	30	6.8
☐	tr Q6C7M8	_YARLI Similar to sp|P38778 Saccharomyces cerevisiae Tr...	30	6.8
☐	tr Q4SLL1	_TETNG Chromosome 15 SCAF14556, whole genome shotgun se...	29	9.1

☐	tr	Q3T8J2	_9NIDO	Polyprotein 1ab [pol1ab] [Breda virus]	29 9.1
☐	tr	Q3T8J1	_9NIDO	Replicase [ORF1a] [Breda virus]	29 9.1
☐	tr	Q81LL9	_BACAN	Iron compound ABC transporter, iron compound-bin...	29 9.1
☐	tr	Q6HDF6	_BACHK	Iron compound ABC transporter, iron compound-bin...	29 9.1
☐	tr	Q634H5	_BACCZ	Iron compound ABC transporter, iron compound-bin...	29 9.1
☐	tr	Q8R7D3	_THETN	Membrane-associated lipoprotein involved in thia...	29 9.1
☐	tr	Q818A5	_BACCR	Ferrichrome-binding protein [BC4363] [Bacillus c...	29 9.1
☐	tr	Q73K80	_TREDE	FMN-binding domain protein [TDE2340] [Treponema ...	29 9.1
☐	tr	Q730G6	_BACC1	Iron compound ABC transporter, iron compound-bin...	29 9.1
☐	tr	Q72R00	_LEPIC	Hypothetical protein [LIC11952] [Leptospira inte...	29 9.1
☐	tr	Q4MRX0	_BACCE	Ferrichrome-binding protein [BCE_G9241_4421] [Ba...	29 9.1
☐	tr	Q4HL84	_CAMLA	Hypothetical protein [CLA0484] [Campylobacter la...	29 9.1
☐	tr	Q08858	_KLEPN	Fimbrial adhesin precursor [fimH] [Klebsiella pn...	29 9.1
☐	tr	Q7RJ39	_PLAYO	Hypothetical protein [PY03425] [Plasmodium yoeli...	29 9.1

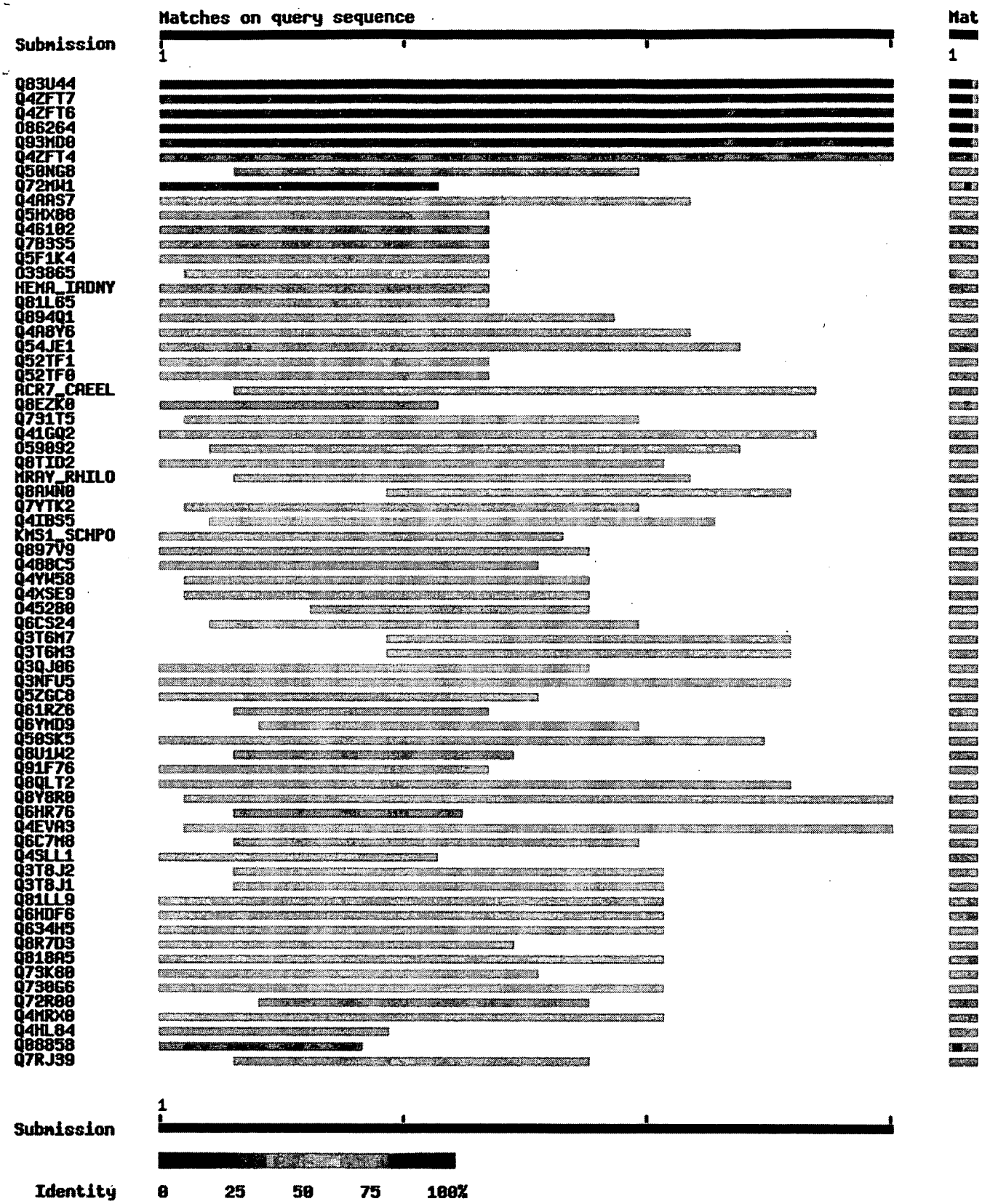
Graphical overview of the alignments

Click here to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(? Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits


Matches on query sequence
Mat
Submission
1
1
Q83U44
Q4ZFT7
Q4ZFT6
O86264
Q93MD0
Q4ZFT4
Q50NG8
Q72MW1
Q4AAS7
Q5HX88
Q46102
Q7B3S5
Q5F1K4
O33865
HEMA_IADNY
Q81L65
Q894Q1
Q4A8Y6
Q54JE1
Q52TF1
Q52TF0
ACR7_CAEEL
Q8EZK0
Q731T5
Q41GQ2
O59092
Q8TID2
MRAY_RHILO
Q8AWN0
Q7YTK2
Q4IBS5
KMS1_SCHPO
Q897V9
Q488C5
Q4YW58
Q4XSE9
O45280
Q6CS24
Q3T6M7
Q3T6M3
Q3QJ86
Q3NFU5
Q5ZGC8
Q61RZ6
Q6YMD9
Q58SK5
Q8U1W2
Q91F76
Q8QLT2
Q8Y8R0
Q6HR76
Q4EVA3
Q6C7M8
Q4SLL1
Q3T8J2
Q3T8J1
Q81LL9
Q6HDF6
Q634H5
Q8R7D3
Q818A5
Q73K80
Q730G6
Q72R80
Q4MRX0
Q4HL84
Q88858
Q7RJ39
1
Submission
Identity
0
25
50
75
100%

Alignments

tr Q83U44 **Beta2-toxin [cpb2] [Clostridium perfringens]** 265 AA
Q83U44_CLOPE
align

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

```
Query: 1  MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
          MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
```

tr Q4ZFT7 **Beta2 toxin [Clostridium perfringens]** 265 AA
Q4ZFT7_CLOPE
align

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

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Query: 1  MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
          MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
```

tr Q4ZFT6 **Beta2 toxin [Clostridium perfringens]** 265 AA
Q4ZFT6_CLOPE
align

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

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Query: 1  MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
          MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
```

tr O86264 **Beta 2 toxin precursor [Clostridium perfringens C]** 265 AA
O86264_CLOPE
align

Score = 94.8 bits (216), Expect = 2e-19
Identities = 29/30 (96%), Positives = 29/30 (96%)

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Query: 1  MKKIISLFTVIFMFSCFLIVGAISPMKASA 30
          MKKIIS FTVIFMFSCFLIVGAISPMKASA
Sbjct: 1  MKKIISKFTVIFMFSCFLIVGAISPMKASA 30
```

tr Q93MD0 **Beta2-toxin [cpb2] [Clostridium perfringens]** 265 AA
Q93MD0_CLOPE
align

UniProtKB/Swiss-Prot entry P09870

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

Entry information

Entry name	**CLOS_CLOHI**
Primary accession number	**P09870**
Secondary accession number	P09869
Entered in Swiss-Prot in	Release 10, March 1989
Sequence was last modified in	Release 26, July 1993
Annotations were last modified in	Release 49, January 2006

Name and origin of the protein

Protein name	**Alpha-clostripain [Precursor]**
Synonyms	**EC 3.4.22.8** **Clostridiopeptidase B**
Contains	**Alpha-clostripain light chain** **Alpha-clostripain heavy chain**
Gene name	**Name: cloSI**
From	Clostridium histolyticum [TaxID: 1498]
Taxonomy	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].
DOI=10.1007/BF00276893; PubMed=8341259 [NCBI, ExPASy, EBI, Israel, Japan]
Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;
"The heterodimeric protease clostripain from Clostridium histolyticum is encoded by a single gene.";
Mol. Gen. Genet. 240:140-145(1993).

[2] PROTEIN SEQUENCE OF 51-181.
PubMed=6391922 [NCBI, ExPASy, EBI, Israel, Japan]
Gilles A.M., Lecroisey A., Keil B.;
"Primary structure of alpha-clostripain light chain.";
Eur. J. Biochem. 145:469-476(1984).

[3] PRELIMINARY PROTEIN SEQUENCE OF 51-73 AND 191-232.
PubMed=6337850 [NCBI, ExPASy, EBI, Israel, Japan]
Gilles A.M., de Wolf A., Keil B.;
"Amino-acid sequences of the active-site sulfhydryl peptide and other thiol peptides from the cysteine proteinase alpha-clostripain.";
Eur. J. Biochem. 130:473-479(1983).

Comments

- ***FUNCTION***: Cysteine endopeptidase with strict specificity.
- ***CATALYTIC ACTIVITY***: Preferential cleavage: Arg-|-Xaa, including Arg-|-Pro bond, but not Lys-|-Xaa.
- ***SUBUNIT***: Heterodimer of a light chain and an heavy chain held together by strong noncovalent forces rather than by intramolecular disulfide bridges.
- ***SIMILARITY***: Belongs to the peptidase C11 family [view classification].
- ***DATABASE***: NAME=Worthington enzyme manual; WWW="http://www.worthington-biochem.com/CP/".

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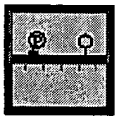
Cross-references

EMBL	X63673; CAA45212.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A29174; A29174. A29175; A29175. B29175; B29175. S35190; S35190.	
MEROPS	C11.001; -.	
InterPro	IPR005077; Peptidase_C11. Graphical view of domain structure.	
Pfam	PF03415; Peptidase_C11; 1. Pfam graphical view of domain structure.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
BLOCKS	P09870.	
ProtoNet	P09870.	
ProtoMap	P09870.	
PRESAGE	P09870.	
DIP	P09870.	
ModBase	P09870.	
SWISS-2DPAGE	Get region on 2D PAGE.	
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.	

Keywords

Direct protein sequencing; Hydrolase; Protease; Signal; Thiol protease; Zymogen.

Features

 Feature table viewer

Feature aligner

Key	From	To	Length	Description	FTId
SIGNAL	1	27	27	*Potential.*	
PROPEP	28	50	23	*Potential.*	PRO_0000028511
CHAIN	51	181	131	Alpha-clostripain light chain.	PRO_0000028512
PROPEP	182	190	9	Linker.	PRO_0000028513
CHAIN	191	526	336	Alpha-clostripain heavy chain.	PRO_0000028514

ACT_SITE	231	231	
CONFLICT	127	127	R -> NQL (in Ref. 2).
CONFLICT	176	179	HGGG -> GDGH (in Ref. 2).
CONFLICT	197	197	S -> H (in Ref. 3).
CONFLICT	213	213	I -> L (in Ref. 3).
CONFLICT	216	216	H -> T (in Ref. 3).
CONFLICT	232	232	L -> M (in Ref. 3).

Sequence information

Length: **526 AA** [This is the length of the unprocessed precursor]

Molecular weight: **59733 Da** [This is the MW of the unprocessed precursor]

CRC64: **E151372FF6C95BE7** [This is a checksum on the sequence]

```
        10         20         30         40         50         60
MLRRKVSTLL MTALITTSFL NSKPVYANPV TKSKDNNLKE VQQVTSKSNK NKNQKVTIMY

        70         80         90        100        110        120
YCDADNNLEG SLLNDIEEMK TGYKDSPNLN LIALVDRSPR YSSDEKVLGE DFSDTRLYKI

       130        140        150        160        170        180
EHNKANRLDG KNEFPEISTT SKYEANMGDP EVLKKFIDYC KSNYEADKYV LIMANHGGGA

       190        200        210        220        230        240
REKSNPRLNR AICWDDSNLD KNGEADCLYM GEISDHLTEK QSVDLLAFDA CLMGTAEVAY

       250        260        270        280        290        300
QYRPGNGGFS ADTLVASSPV VWGPGFKYDK IFDRIKAGGG TNNEDDLTLG GKEQNFDPAT

       310        320        330        340        350        360
ITNEQLGALF VEEQRDSTHA NGRYDQHLSF YDLKKAESVK RAIDNLAVNL SNENKKSEIE

       370        380        390        400        410        420
KLRGSGIHTD LMHYFDEYSE GEWVEYPYFD VYDLCEKINK SENFSSKTKD LASNAMNKLN

       430        440        450        460        470        480
EMIVYSFGDP SNNFKEGKNG LSIFLPNGDK KYSTYYTSTK IPHWTMQSWY NSIDTVKYGL

       490        500        510        520
NPYGKLSWCK DGQDPEINKV GNWFELLDSW FDKTNDVTGG VNHYQW
```

P09870 in FASTA format

View entry in original UniProtKB/Swiss-Prot format
View entry in raw text format (no links)
Report form for errors/updates in this UniProtKB/Swiss-Prot entry

BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

ExPASy Home page **Site Map** **Search ExPASy** **Contact us** **Swiss-Prot**
Hosted by SIB Switzerland Mirror sites: Australia Brazil Canada Korea Taiwan USA

EMBL-EBI
European Bioinformatics Institute

Entry Information

Entry from: EMBL

Entry Options

Launch analysis tool:

BlastN Launch

Link to related information: Link

Save entry: Save

View: Printer Friendly

Go to: General Description References Additional Sequence

General Information

Primary Accession #	X63673
Accession #	X63673
Entry Name	EMBL:CHCLOSI
Molecule Type	genomic DNA
Sequence Length	2768
Entry Division	PRO
Sequence Version	X63673.1
Creation Date	21-FEB-1992
Modification Date	19-JUL-1993

Description

Description	C.histolyticum closI gene for alpha-clostripain
Keywords	closI gene; Clostripain.;
Organism	Clostridium histolyticum
Organism Classification	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiacea

References

1. Diefenthal,T.;

   Submitted (28-JAN-1992) to the EMBL/GenBank/DDBJ dat
   Research, Dept. Biotechnology, Schaarstr.1, P.O.B. 20 65,

   Position 1-2368

2. Dargatz,H.; Diefenthal,T.; Witte,V.; Reipen,G.; von Wettst
   The heterodimeric protease clostripain from Clostrid single gene
   Mol. Gen. Genet. 240(1):140-145 (1993)

   DOI 10.1007/BF00276893

   Pubmed 8341259

   Position 1-2368

Additional Information

Features

Key	Location	Qualifier	Value
source	1..2768	db_xref	taxon:1498
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		organism	Clostridium histolyti
-35_signal	376..381		
-10_signal	397..402		
repeat_region	420..438	note	palindrom-structure
		rpt_type	INVERTED
rbs	605..609		
cds	618..2198	db_xref	GOA:P09870
		db_xref	InterPro:IPR0050
		db_xref	UniProtKB/Swiss-I
		transl_table	11
		gene	ClosI
		EC_number	3.4.22.8
		product	clostripain
		protein_id	CAA45212.1
		translation	>CAA45212 MLRRKVSTLLMTALI YCDADNNLEGSLLNI EHNKANRLDGKNEFI REKSNPRLNRAICWI

Sequence

Characteristics **Length:** 2768 BP, **A Count:**1084, **C Count:**359, **G Count**

Sequence

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tgaagcacttgccgataaaactgcacttaacatccaaagatggc
gagtatct
```

Go to: General Description References Additional Sequence

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Entry Options

Launch analysis tool:

BlastN

Launch

Link to related information:

Link

Save entry: Save

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```
ID   CHCLOSI_2; parent: CHCLOSI
AC   X63673;
FT   -35_signal       376..381
SQ   Sequence     6 BP;
     ttgtaa
//
```

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Entry from: EMBL_features

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ID   CHCLOSI_3; parent: CHCLOSI
AC   X63673;
FT   -10_signal       397..402
SQ   Sequence      6 BP;
     tataat
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Entry Options

Launch analysis tool:

BlastN

Launch

Link to related information:

Link

Save entry: Save

View:

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Entry Information

Entry from: EMBL_features

Entry Options

Launch analysis tool:

BlastN

Launch

Link to related information:

Link

Save entry: Save

View:

Printer Friendly

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FT                    /note="palindrom-structure"
FT                    /rpt_type=INVERTED
SQ   Sequence    19 BP;
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ID   CLOS_CLOHI     STANDARD;      PRT;   526 AA.
AC   P09870; P09869;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   24-JAN-2006 (Rel. 49, Last annotation update)
DE   Alpha-clostripain precursor (EC 3.4.22.8) (Clostridiopeptidase B)
DE   [Contains: Alpha-clostripain light chain; Alpha-clostripain heavy
DE   chain].
GN   Name=cloSI;
OS   Clostridium histolyticum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1498;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=93341452; PubMed=8341259; DOI=10.1007/BF00276893;
RA   Dargatz H., Diefenthal T., Witte V., Reipen G., von Wettstein D.;
RT   "The heterodimeric protease clostripain from Clostridium histolyticum
RT   is encoded by a single gene.";
RL   Mol. Gen. Genet. 240:140-145(1993).
RN   [2]
RP   PROTEIN SEQUENCE OF 51-181.
RX   MEDLINE=85076641; PubMed=6391922;
RA   Gilles A.M., Lecroisey A., Keil B.;
RT   "Primary structure of alpha-clostripain light chain.";
RL   Eur. J. Biochem. 145:469-476(1984).
RN   [3]
RP   PRELIMINARY PROTEIN SEQUENCE OF 51-73 AND 191-232.
RX   MEDLINE=83131688; PubMed=6337850;
RA   Gilles A.M., de Wolf A., Keil B.;
RT   "Amino-acid sequences of the active-site sulfhydryl peptide and other
RT   thiol peptides from the cysteine proteinase alpha-clostripain.";
RL   Eur. J. Biochem. 130:473-479(1983).
CC   -!- FUNCTION: Cysteine endopeptidase with strict specificity.
CC   -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, including
CC       Arg-|-Pro bond, but not Lys-|-Xaa.
CC   -!- SUBUNIT: Heterodimer of a light chain and an heavy chain held
CC       together by strong noncovalent forces rather than by
CC       intramolecular disulfide bridges.
CC   -!- SIMILARITY: Belongs to the peptidase C11 family.
CC   -!- DATABASE: NAME=Worthington enzyme manual;
CC       WWW="http://www.worthington-biochem.com/CP/".
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X63673; CAA45212.1; -; Genomic_DNA.
DR   PIR; A29174; A29174.
DR   PIR; A29175; A29175.
DR   PIR; B29175; B29175.
DR   PIR; S35190; S35190.
DR   MEROPS; C11.001; -.
DR   InterPro; IPR005077; Peptidase_C11.
DR   Pfam; PF03415; Peptidase_C11; 1.
KW   Direct protein sequencing; Hydrolase; Protease; Signal;
KW   Thiol protease; Zymogen.
FT   SIGNAL        1     27       Potential.
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FT   PROPEP        28     50       Potential.
FT                                 /FTId=PRO_0000028511.
FT   CHAIN         51    181       Alpha-clostripain light chain.
FT                                 /FTId=PRO_0000028512.
FT   PROPEP       182    190       Linker.
FT                                 /FTId=PRO_0000028513.
FT   CHAIN        191    526       Alpha-clostripain heavy chain.
FT                                 /FTId=PRO_0000028514.
FT   ACT_SITE     231    231
FT   CONFLICT     127    127       R -> NQL (in Ref. 2).
FT   CONFLICT     176    179       HGGG -> GDGH (in Ref. 2).
FT   CONFLICT     197    197       S -> H (in Ref. 3).
FT   CONFLICT     213    213       I -> L (in Ref. 3).
FT   CONFLICT     216    216       H -> T (in Ref. 3).
FT   CONFLICT     232    232       L -> M (in Ref. 3).
SQ   SEQUENCE   526 AA;  59733 MW;  E151372FF6C95BE7 CRC64;
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     YCDADNNLEG SLLNDIEEMK TGYKDSPNLN LIALVDRSPR YSSDEKVLGE DFSDTRLYKI
     EHNKANRLDG KNEFPEISTT SKYEANMGDP EVLKKFIDYC KSNYEADKYV LIMANHGGGA
     REKSNPRLNR AICWDDSNLD KNGEADCLYM GEISDHLTEK QSVDLLAFDA CLMGTAEVAY
     QYRPGNGGFS ADTLVASSPV VWGPGFKYDK IFDRIKAGGG TNNEDDLTLG GKEQNFDPAT
     ITNEQLGALF VEEQRDSTHA NGRYDQHLSF YDLKKAESVK RAIDNLAVNL SNENKKSEIE
     KLRGSGIHTD LMHYFDEYSE GEWVEYPYFD VYDLCEKINK SENFSSKTKD LASNAMNKLN
     EMIVYSFGDP SNNFKEGKNG LSIFLPNGDK KYSTYYTSTK IPHWTMQSWY NSIDTVKYGL
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FT                   /mol_type="genomic DNA"
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     gagtatct
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AC   L77965;
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SV   L77965.1
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DT   28-JUL-1998 (Rel. 56, Created)
DT   29-JUL-1998 (Rel. 56, Last updated, Version 2)
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DE   Clostridium perfringens C beta 2 toxin gene, complete cds.
XX
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OS   Clostridium perfringens C
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
XX
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RP   1-1392
RX   DOI; 10.1016/S0378-1119(97)00493-9
RX   PUBMED; 9426008.
RA   Gibert M., Jolivet-Reynaud C., Popoff M.R.;
RT   "Beta2 toxin, a novel toxin produced by Clostridium perfringens";
RL   Gene 203(1):65-73(1997).
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RN   [2]
RP   1-1392
RA   Popoff M.R.;
RT   ;
RL   Submitted (15-JAN-1998) to the EMBL/GenBank/DDBJ databases.
RL   Toxines Microbiennes, Institut Pasteur, Paris cedex 15 75724, France
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CC   [Flatfile retrieved from GSDB Fri Jul 24 15:39:17 1998].
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